

SEQUENCE LISTING

<110> Oy Jurilab Ltd

<120> Method for detecting the risk of acute myocardial infarction and coronary heart disease

<130> 40597

<160> 56

<170> PatentIn version 3.1

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 Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
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 gtc atc ctg gct gtg ttg acc agc cgc tcg ctg cgc gcc cct cag aac 144
 Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
 35 40 45
 ctg ttc ctg gtg tcg ctg gcc gcc gcc gac atc ctg gtg gcc acg ctc 192
 Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
 50 55 60
 atc atc cct ttc tcg ctg gcc aac gag ctg ctg ggc tac tgg tac ttc 240
 Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
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 Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
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 gcc gtg agc cgc gcg ctg gag tac aac tcc aag cgc acc ccg cgc cgc 384
 Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
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 Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
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Cys	Gly 290	Ala	Ser	Pro	Glu	Asp 295	Glu	Ala	Glu	Glu	Glu	Glu	Glu	Glu	Glu	
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Val	Leu 370	Ala	Val	Val	Ile 375	Gly	Val	Phe	Val	Leu	Cys 380	Trp	Phe	Pro	Phe	
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 Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg
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Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu
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Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg Phe Thr Phe
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Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe
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 385 390 395 400

Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser

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Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu	20	25	30	
gtc atc ctg gct gtg ttg acc agc cgc tcg ctg cgc gcc cct cag aac				144
Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn	35	40	45	
ctg ttc ctg gtg tcg ctg gcc gcc gcc gac atc ctg gtg gcc acg ctc				192
Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu	50	55	60	
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Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe	65	70	75	80
cgg cgc acg tgg tgc gag gtg tac ctg gcg ctc gac gtg ctc ttc tgc				288
Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys	85	90	95	
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Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp	100	105	110	
gcc gtg agc cgc gcg ctg gag tac aac tcc aag cgc acc ccg cgc cgc				384
Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg	115	120	125	
atc aag tgc atc atc ctc act gtg tgg ctc atc gcc gcc gtc atc tcg				432
Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser	130	135	140	
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Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr	180 185 190
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Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp	210 215 220
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His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val	225 230 235 240
gct tct gcc aga gag gtc aac gga cac tcg aag tcc act ggg gag aag	768
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Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val	275 280 285
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Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
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Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
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His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val
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Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
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Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu
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Glu Glu Glu Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala
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aaccaaagca gtgcaagatt cagttcaagg tcctgaaaaa agaaaaacat ttactctgt 480
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tgtttgacct ttttaatttt cttttctttt tccttttttt tcttttgctt tgttatatgg 600
tggtttgtat ggttccttt 619

```

```

<210> 28
<211> 619
<212> DNA
<213> Homo sapiens
<400> 28

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```

ggatgaagca gaatgaagag taggtaaccc tgagggtgag aggtatattg ttggaccagg 60
gagcaggtaa taaatacatc ctggatagac tcacatgggg aaaaaaacta tgatcttgca 120
tgactaacac atagctagta agatttcttg tcacttacga caaagacatg aattttctcc 180
atcctaacat gactgataca gtgtctctta tttagactat ctcagttagt ctggctgtgc 240
ttgtcctttt tcccacctcc ctgctgtgct ctgacctctt cttctttcca caggttctca 300
ggcaagagcc acctgctatt gccgaaccgg ccgttggtgt acccgtgagt ccctctccgg 360
ggtgtgtgaa atcagtggcc gcctctacag actctgctgt cgctgagctt cctagataga 420
aaccaaagca gtgcaagatt cagttcaagg tcctgaaaaa agaaaaacat ttactctgt 480
gtaccttggtg tctttctaaa tttctctctc caaaataaag ttcaagcatt aaacttagtg 540
tgtttgacct ttttaatttt cttttctttt tccttttttt tcttttgctt tgttatatgg 600
tggtttgtat ggttccttt 619

```

```

<210> 29
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 29
ggatgaagca gaatgaaga 19

```

```

<210> 30
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 30

```

aaaggaacca tacaaacca

19

<210> 31
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Sequencing primer
 <400> 31
 gttagtctgg ctgtgctt

18

<210> 32
 <211> 1052
 <212> DNA
 <213> Homo sapiens
 <400> 32
 gggctactga gtttggtgaa aagataagac tcctgaaaat tctattgatt ctcttttgaa 60
 cttcttttctt aaattagttt tatgatggac ttggctctca ttggtatttc ccaagattat 120
 ggagatggga tagtgatgtc tgacaagtac ctaagatgct aagttgaagg tctaaaattc 180
 catcctaaaa gcaaataatt actctatcat ctacgtgccc tttgcttctt aaagttactc 240
 aaggaaggca gactaaacag gaaatttact ttggattcaa gaggggcata gagacgctct 300
 cagcctgccc atttgccctc atcaacattc ctaaacactg ggcttaaaat gtagtatgag 360
 taaactctct cttagtctat ccatctccca ctagcagttt taacatcatc tctagttatt 420
 aaccttggtc caatggcttt ctccctctttt ttatatacaga atttattggc ttgagacgct 480
 gtttaaatggg tttggggaga tgcagggatc actgcaatgt ggatgaaaaa gagatacaga 540
 aatgcaagat gaaaaaatgt tgtgttggac caaagtggg taaattgatt aaaaactacc 600
 tgcaatatgg aacaccaa atgtacttaatg aagacgtcca agaaatgcta aaacctgcc 660
 agaattctag tgctgtgata caaagaaaac atattttatac tgttctcccc caaatcaaaa 720
 gcactagctt ttttgcta atccaactttg tcatcattcc aaatgccacc cctatgaact 780
 ctgccaccat cagcactatg accccaggac agatcacata cactgctact tctaccaaga 840
 gtaacaccaa agaaagcaga gattctgcc ctgcctcgcc accaccagca ccacctccac 900
 caaacatact gccaacacca tcaactggagc tagaggaagc agaagagcag taatgtggat 960
 ctttccctta aaactccaag ttccctctcta tttttgctat ctataaaatg acatagaact 1020
 gtttcctctg tcatcagtc ttcaataaac ac 1052

<210> 33
 <211> 1049
 <212> DNA
 <213> Homo sapiens
 <400> 33

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gggctactga gtttggtgaa aagataagac tcctgaaaat tctattgatt ctcttttgaa      60
cttcttttctt aaattagttt tatgatggac ttggctctca ttggtatttc ccaagattat      120
ggagatggga tagtgatgtc tgacaagtac ctaagatgct aagttgaagg tctaaaattc      180
catcctaaaa gcaaataatt actctatcat ctacgtgccc tttgcttctt aaagttactc      240
aaggaaggca gactaaacag gaaatttact ttggattcaa gaggggcata gagacgctct      300
cagcctgccc atttgccttc atcaacattc ctaaactctg ggcttaaaat gtagtatgag      360
taaactctct cttagtctat ccatctccca ctagcagttt taacatcatc tctagttatt      420
aaccttggct caatggcttt ctcttttttt atacagaatt tattggcttg agacgctggt      480
taatgggttt ggggagatgc agggatcact gcaatgtgga tgaaaaagag atacagaaat      540
gcaagatgaa aaaatgttgt gttggaccaa aagtggttta attgattaaa aactacctgc      600
aatatggaac accaaatgta cttaatgaag acgtccaaga aatgctaaaa cctgccaaaga      660
attctagtgc tgtgatacaa agaaaacata ttttatctgt tctcccccaa atcaaaagca      720
ctagcttttt tgctaatacc aactttgtca tcattccaaa tgccaccctt atgaactctg      780
ccaccatcag cactatgacc ccaggacaga tcacatacac tgctacttct accaagagta      840
acaccaaaga aagcagagat tctgccactg cctcgccacc accagcacca cctccaccaa      900
acatactgcc aacaccatca ctggagctag aggaagcaga agagcagtaa tgtggatctt      960
tcccttaaaa ctccaagttc ctctctattt ttgctatcta taaaatgaca tagaactggt      1020
tcctctgtca tcagtcattc aataaacac                                     1049

```

```

<210> 34
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 34
ggctactgag tttggtga

```

18

```

<210> 35
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 35
gtgtttattg aatgactgat g

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21

```

<210> 36
<211> 18
<212> DNA
<213> Artificial Sequence

```


<220>
 <223> Sequencing primer
 <400> 36
 caaggaaggc agactaaa 18

<210> 37
 <211> 552
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1)..(552)
 <223> Coding sequence for the variant human DEFB129 gene
 <400> 37

atg aag ctc ctt ttt cct atc ttt gcc agc ctc atg cta cag tac cag 48
 Met Lys Leu Leu Phe Pro Ile Phe Ala Ser Leu Met Leu Gln Tyr Gln
 1 5 10 15

gtg aac aca gaa ttt att ggc ttg aga cgc tgt tta atg ggt ttg ggg 96
 Val Asn Thr Glu Phe Ile Gly Leu Arg Arg Cys Leu Met Gly Leu Gly
 20 25 30

aga tgc agg gat cac tgc aat gtg gat gaa aaa gag ata cag aaa tgc 144
 Arg Cys Arg Asp His Cys Asn Val Asp Glu Lys Glu Ile Gln Lys Cys
 35 40 45

aag atg aaa aaa tgt tgt gtt gga cca aaa gtg gtt aaa ttg att aaa 192
 Lys Met Lys Lys Cys Cys Val Gly Pro Lys Val Val Lys Leu Ile Lys
 50 55 60

aac tac ctg caa tat gga aca cca aat gta ctt aat gaa gac gtc caa 240
 Asn Tyr Leu Gln Tyr Gly Thr Pro Asn Val Leu Asn Glu Asp Val Gln
 65 70 75 80

gaa atg cta aaa cct gcc aag aat tct agt gct gtg ata caa aga aaa 288
 Glu Met Leu Lys Pro Ala Lys Asn Ser Ser Ala Val Ile Gln Arg Lys
 85 90 95

cat att tta tct gtt ctc ccc caa atc aaa agc act agc ttt ttt gct 336
 His Ile Leu Ser Val Leu Pro Gln Ile Lys Ser Thr Ser Phe Phe Ala
 100 105 110

aat acc aac ttt gtc atc att cca aat gcc acc cct atg aac tct gcc 384
 Asn Thr Asn Phe Val Ile Ile Pro Asn Ala Thr Pro Met Asn Ser Ala
 115 120 125

acc atc agc act atg acc cca gga cag atc aca tac act gct act tct 432
 Thr Ile Ser Thr Met Thr Pro Gly Gln Ile Thr Tyr Thr Ala Thr Ser
 130 135 140

acc aag agt aac acc aaa gaa agc aga gat tct gcc act gcc tcg cca 480
 Thr Lys Ser Asn Thr Lys Glu Ser Arg Asp Ser Ala Thr Ala Ser Pro
 145 150 155 160

cca cca gca cca cct cca cca aac ata ctg cca aca cca tca ctg gag 528
 Pro Pro Ala Pro Pro Pro Pro Asn Ile Leu Pro Thr Pro Ser Leu Glu
 165 170 175

cta gag gaa gca gaa gag cag taa 552
 Leu Glu Glu Ala Glu Glu Gln

180

<210> 38
 <211> 183
 <212> PRT
 <213> Homo sapiens
 <400> 38

Met Lys Leu Leu Phe Pro Ile Phe Ala Ser Leu Met Leu Gln Tyr Gln
 1 5 10 15

Val Asn Thr Glu Phe Ile Gly Leu Arg Arg Cys Leu Met Gly Leu Gly
 20 25 30

Arg Cys Arg Asp His Cys Asn Val Asp Glu Lys Glu Ile Gln Lys Cys
 35 40 45

Lys Met Lys Lys Cys Cys Val Gly Pro Lys Val Val Lys Leu Ile Lys
 50 55 60

Asn Tyr Leu Gln Tyr Gly Thr Pro Asn Val Leu Asn Glu Asp Val Gln
 65 70 75 80

Glu Met Leu Lys Pro Ala Lys Asn Ser Ser Ala Val Ile Gln Arg Lys
 85 90 95

His Ile Leu Ser Val Leu Pro Gln Ile Lys Ser Thr Ser Phe Phe Ala
 100 105 110

Asn Thr Asn Phe Val Ile Ile Pro Asn Ala Thr Pro Met Asn Ser Ala
 115 120 125

Thr Ile Ser Thr Met Thr Pro Gly Gln Ile Thr Tyr Thr Ala Thr Ser
 130 135 140

Thr Lys Ser Asn Thr Lys Glu Ser Arg Asp Ser Ala Thr Ala Ser Pro
 145 150 155 160

Pro Pro Ala Pro Pro Pro Pro Asn Ile Leu Pro Thr Pro Ser Leu Glu
 165 170 175

Leu Glu Glu Ala Glu Glu Gln
 180

<210> 39
 <211> 552
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(552)
 <223> Coding sequence for the human DEFB129 gene
 <400> 39
 atg aag ctc ctt ttt cct atc ttt gcc agc ctc atg cta cag tac cag 48
 Met Lys Leu Leu Phe Pro Ile Phe Ala Ser Leu Met Leu Gln Tyr Gln
 1 5 10 15
 gtg aac aca gaa ttt att ggc ttg aga cgc tgt tta atg ggt ttg ggg 96
 Val Asn Thr Glu Phe Ile Gly Leu Arg Arg Cys Leu Met Gly Leu Gly
 20 25 30
 aga tgc agg gat cac tgc aat gtg gat gaa aaa gag ata cag aaa tgc 144
 Arg Cys Arg Asp His Cys Asn Val Asp Glu Lys Glu Ile Gln Lys Cys
 35 40 45
 aag atg aaa aaa tgt tgt gtt gga cca aaa gtg gtt aaa ttg att aaa 192
 Lys Met Lys Lys Cys Cys Val Gly Pro Lys Val Val Lys Leu Ile Lys
 50 55 60
 aac tac cta caa tat gga aca cca aat gta ctt aat gaa gac gtc caa 240
 Asn Tyr Leu Gln Tyr Gly Thr Pro Asn Val Leu Asn Glu Asp Val Gln
 65 70 75 80
 gaa atg cta aaa cct gcc aag aat tct agt gct gtg ata caa aga aaa 288
 Glu Met Leu Lys Pro Ala Lys Asn Ser Ser Ala Val Ile Gln Arg Lys
 85 90 95
 cat att tta tct gtt ctc ccc caa atc aaa agc act agc ttt ttt gct 336
 His Ile Leu Ser Val Leu Pro Gln Ile Lys Ser Thr Ser Phe Phe Ala
 100 105 110
 aat acc aac ttt gtc atc att cca aat gcc acc cct atg aac tct gcc 384
 Asn Thr Asn Phe Val Ile Ile Pro Asn Ala Thr Pro Met Asn Ser Ala
 115 120 125
 acc atc agc act atg acc cca gga cag atc aca tac act gct act tct 432
 Thr Ile Ser Thr Met Thr Pro Gly Gln Ile Thr Tyr Thr Ala Thr Ser
 130 135 140
 acc aag agt aac acc aaa gaa agc aga gat tct gcc act gcc tcg cca 480
 Thr Lys Ser Asn Thr Lys Glu Ser Arg Asp Ser Ala Thr Ala Ser Pro
 145 150 155 160
 cca cca gca cca cct cca cca aac ata ctg cca aca cca tca ctg gag 528
 Pro Pro Ala Pro Pro Pro Pro Asn Ile Leu Pro Thr Pro Ser Leu Glu
 165 170 175
 cta gag gaa gca gaa gag cag taa 552
 Leu Glu Glu Ala Glu Glu Gln
 180
 <210> 40
 <211> 183
 <212> PRT
 <213> Homo sapiens
 <400> 40

Met Lys Leu Leu Phe Pro Ile Phe Ala Ser Leu Met Leu Gln Tyr Gln

1	5	10	15
Val Asn Thr	Glu Phe Ile Gly Leu Arg	Arg Cys Leu Met	Gly Leu Gly
	20	25	30
Arg Cys Arg	Asp His Cys Asn Val Asp	Glu Lys Glu Ile	Gln Lys Cys
	35	40	45
Lys Met Lys	Lys Cys Cys Val Gly Pro	Lys Val Val Lys	Leu Ile Lys
	50	55	60
Asn Tyr Leu	Gln Tyr Gly Thr Pro Asn	Val Leu Asn Glu Asp	Val Gln
	65	70	75
Glu Met Leu	Lys Pro Ala Lys Asn Ser	Ser Ala Val Ile	Gln Arg Lys
	85	90	95
His Ile Leu	Ser Val Leu Pro Gln Ile	Lys Ser Thr Ser	Phe Phe Ala
	100	105	110
Asn Thr Asn	Phe Val Ile Ile Pro Asn	Ala Thr Pro Met	Asn Ser Ala
	115	120	125
Thr Ile Ser	Thr Met Thr Pro Gly Gln	Ile Thr Tyr Thr	Ala Thr Ser
	130	135	140
Thr Lys Ser	Asn Thr Lys Glu Ser Arg	Asp Ser Ala Thr	Ala Ser Pro
	145	150	155
Pro Pro Ala	Pro Pro Pro Asn Ile Leu	Pro Thr Pro Ser	Leu Glu
	165	170	175
Leu Glu Glu	Ala Glu Glu Gln		
	180		

<210> 41

<211> 372

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(372)

<223> Coding sequence for the variant human DEFB118 gene

<400> 41

atg aaa ctc	ctg ctg ctg gct	ctt cct atg	ctt gtg ctc	cta ccc caa	48
Met Lys Leu	Leu Leu Ala Leu	Pro Met Leu	Val Leu Leu	Pro Gln	
1	5	10	15		

gtg atc cca	gcc tat agt	ggt gaa aaa	aaa tgc	tgg aac	aga tca	ggg	96
-------------	-------------	-------------	---------	---------	---------	-----	----

Val Ile Pro Ala Tyr Ser Gly Glu Lys Lys Cys Trp Asn Arg Ser Gly
20 25 30

cac cgc agg aaa caa tgc aaa gat gga gaa gca gtg aaa gat aca tgc 144
His Arg Arg Lys Gln Cys Lys Asp Gly Glu Ala Val Lys Asp Thr Cys
35 40 45

aaa aat ctt cga gct tgc tgc att cca tcc aat gaa gac cac agg cga 192
Lys Asn Leu Arg Ala Cys Cys Ile Pro Ser Asn Glu Asp His Arg Arg
50 55 60

gtt cct gcg aca tct ccc aca ccc ttg agt gac tca aca cca gga att 240
Val Pro Ala Thr Ser Pro Thr Pro Leu Ser Asp Ser Thr Pro Gly Ile
65 70 75 80

att gat gat att tta aca gta agg ttc acg aca gac tac ttt gaa gta 288
Ile Asp Asp Ile Leu Thr Val Arg Phe Thr Thr Asp Tyr Phe Glu Val
85 90 95

agc agc aag aaa gat atg gtt gaa gag tct gag gcg gga agg gga act 336
Ser Ser Lys Lys Asp Met Val Glu Glu Ser Glu Ala Gly Arg Gly Thr
100 105 110

gag acc tct ctt cca aat gtt cac cat agc tca tga 372
Glu Thr Ser Leu Pro Asn Val His His Ser Ser
115 120

<210> 42
<211> 123
<212> PRT
<213> Homo sapiens
<400> 42

Met Lys Leu Leu Leu Leu Ala Leu Pro Met Leu Val Leu Leu Pro Gln
1 5 10 15

Val Ile Pro Ala Tyr Ser Gly Glu Lys Lys Cys Trp Asn Arg Ser Gly
20 25 30

His Arg Arg Lys Gln Cys Lys Asp Gly Glu Ala Val Lys Asp Thr Cys
35 40 45

Lys Asn Leu Arg Ala Cys Cys Ile Pro Ser Asn Glu Asp His Arg Arg
50 55 60

Val Pro Ala Thr Ser Pro Thr Pro Leu Ser Asp Ser Thr Pro Gly Ile
65 70 75 80

Ile Asp Asp Ile Leu Thr Val Arg Phe Thr Thr Asp Tyr Phe Glu Val
85 90 95

Ser Ser Lys Lys Asp Met Val Glu Glu Ser Glu Ala Gly Arg Gly Thr
100 105 110

Glu Thr Ser Leu Pro Asn Val His His Ser Ser
 115 120

<210> 43
 <211> 372
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1)..(372)
 <223> Coding sequence of the human DEFB118 gene
 <400> 43

atg aaa ctc ctg ctg ctg gct ctt cct atg ctt gtg ctc cta ccc caa 48
 Met Lys Leu Leu Leu Ala Leu Pro Met Leu Val Leu Leu Pro Gln
 1 5 10 15

gtg atc cca gcc tat agt ggt gaa aaa aaa tgc tgg aac aga tca ggg 96
 Val Ile Pro Ala Tyr Ser Gly Glu Lys Lys Cys Trp Asn Arg Ser Gly
 20 25 30

cac tgc agg aaa caa tgc aaa gat gga gaa gca gtg aaa gat aca tgc 144
 His Cys Arg Lys Gln Cys Lys Asp Gly Glu Ala Val Lys Asp Thr Cys
 35 40 45

aaa aat ctt cga gct tgc tgc att cca tcc aat gaa gac cac agg cga 192
 Lys Asn Leu Arg Ala Cys Cys Ile Pro Ser Asn Glu Asp His Arg Arg
 50 55 60

gtt cct gcg aca tct ccc aca ccc ttg agt gac tca aca cca gga att 240
 Val Pro Ala Thr Ser Pro Thr Pro Leu Ser Asp Ser Thr Pro Gly Ile
 65 70 75 80

att gat gat att tta aca gta agg ttc acg aca gac tac ttt gaa gta 288
 Ile Asp Asp Ile Leu Thr Val Arg Phe Thr Thr Asp Tyr Phe Glu Val
 85 90 95

agc agc aag aaa gat atg gtt gaa gag tct gag gcg gga agg gga act 336
 Ser Ser Lys Lys Asp Met Val Glu Glu Ser Glu Ala Gly Arg Gly Thr
 100 105 110

gag acc tct ctt cca aat gtt cac cat agc tca tga 372
 Glu Thr Ser Leu Pro Asn Val His His Ser Ser
 115 120

<210> 44
 <211> 123
 <212> PRT
 <213> Homo sapiens
 <400> 44

Met Lys Leu Leu Leu Leu Ala Leu Pro Met Leu Val Leu Leu Pro Gln
 1 5 10 15

Val Ile Pro Ala Tyr Ser Gly Glu Lys Lys Cys Trp Asn Arg Ser Gly
 20 25 30

His Cys Arg Lys Gln Cys Lys Asp Gly Glu Ala Val Lys Asp Thr Cys
 35 40 45

Lys Asn Leu Arg Ala Cys Cys Ile Pro Ser Asn Glu Asp His Arg Arg
 50 55 60

Val Pro Ala Thr Ser Pro Thr Pro Leu Ser Asp Ser Thr Pro Gly Ile
 65 70 75 80

Ile Asp Asp Ile Leu Thr Val Arg Phe Thr Thr Asp Tyr Phe Glu Val
 85 90 95

Ser Ser Lys Lys Asp Met Val Glu Glu Ser Glu Ala Gly Arg Gly Thr
 100 105 110

Glu Thr Ser Leu Pro Asn Val His His Ser Ser
 115 120

<210> 45
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> PCR primer
 <400> 45
 aggttgagta tttgccagac

20

<210> 46
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> PCR primer
 <400> 46
 aggacagggg tgagtgata

19

<210> 47
 <211> 246
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1)..(246)
 <223> Coding sequence for the variant human DEFB126 gene
 <400> 47

atg aag tcc cta ctg ttc acc ctt gca gtt ttt atg ctc ctg gcc caa
 Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
 1 5 10 15

48

ttg gtc tca ggt aat tgg tat gtg aaa aag tgt cta aac gac gtt gga
 Leu Val Ser Gly Asn Trp Tyr Val Lys Cys Leu Asn Asp Val Gly
 20 25 30

96

```

att tgc aag aag aag tgc aaa cct gaa gag atg cat gta aag aat ggt      144
Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
      35                      40                      45

tgg gca atg tgc ggc aaa ggg act gct gtg ttc cag ctg aca gac gtg      192
Trp Ala Met Cys Gly Lys Gly Thr Ala Val Phe Gln Leu Thr Asp Val
      50                      55                      60

cta att atc ctg ttt tct gtg tcc aga caa aga cta caa gaa ttt caa      240
Leu Ile Ile Leu Phe Ser Val Ser Arg Gln Arg Leu Gln Glu Phe Gln
      65                      70                      75                      80

cag taa      246
Gln

```

```

<210> 48
<211> 81
<212> PRT
<213> Homo sapiens
<400> 48

```

```

Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
1                      5                      10                      15

```

```

Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
      20                      25                      30

```

```

Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
      35                      40                      45

```

```

Trp Ala Met Cys Gly Lys Gly Thr Ala Val Phe Gln Leu Thr Asp Val
      50                      55                      60

```

```

Leu Ile Ile Leu Phe Ser Val Ser Arg Gln Arg Leu Gln Glu Phe Gln
      65                      70                      75                      80

```

Gln

```

<210> 49
<211> 336
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (1)..(336)
<223> Coding sequence of the human DEFB126 gene
<400> 49

```

```

atg aag tcc cta ctg ttc acc ctt gca gtt ttt atg ctc ctg gcc caa      48
Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
1                      5                      10                      15

```

```

ttg gtc tca ggt aat tgg tat gtg aaa aag tgt cta aac gac gtt gga      96

```



```

Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
      20                      25                      30

att tgc aag aag aag tgc aaa cct gaa gag atg cat gta aag aat ggt      144
Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
      35                      40                      45

tgg gca atg tgc ggc aaa caa agg gac tgc tgt gtt cca gct gac aga      192
Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg
      50                      55                      60

cgt gct aat tat cct gtt ttc tgt gtc cag aca aag act aca aga att      240
Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile
      65                      70                      75                      80

tca aca gta aca gca aca aca gca aca aca act ttg atg atg act act      288
Ser Thr Val Thr Ala Thr Thr Ala Thr Thr Thr Leu Met Met Thr Thr
      85                      90                      95

gct tcg atg tct tcg atg gct cct acc ccc gtt tct ccc act ggt tga      336
Ala Ser Met Ser Ser Met Ala Pro Thr Pro Val Ser Pro Thr Gly
      100                      105                      110

```

```

<210> 50
<211> 111
<212> PRT
<213> Homo sapiens
<400> 50

```

```

Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
1          5          10          15

```

```

Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
      20                      25                      30

```

```

Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
      35                      40                      45

```

```

Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg
      50                      55                      60

```

```

Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile
      65                      70                      75                      80

```

```

Ser Thr Val Thr Ala Thr Thr Ala Thr Thr Thr Leu Met Met Thr Thr
      85                      90                      95

```

```

Ala Ser Met Ser Ser Met Ala Pro Thr Pro Val Ser Pro Thr Gly
      100                      105                      110

```

```

<210> 51
<211> 20
<212> DNA

```

<213> Artificial Sequence
 <220>
 <223> PCR primer
 <400> 51
 aatggtgaga aagatgacag 20

<210> 52
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> PCR primer
 <400> 52
 gttgaatgga gggaaagt 18

<210> 53
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Sequencing primer
 <400> 53
 gtaggtatatt atgattag 18

<210> 54
 <211> 334
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1)..(333)
 <223> Coding sequence for the variant human DEFB126 gene
 <400> 54
 atg aag tcc cta ctg ttc acc ctt gca gtt ttt atg ctc ctg gcc caa 48
 Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
 1 5 10 15

ttg gtc tca ggt aat tgg tat gtg aaa aag tgt cta aac gac gtt gga 96
 Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
 20 25 30

att tgc aag aag aag tgc aaa cct gaa gag atg cat gta aag aat ggt 144
 Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
 35 40 45

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 Trp Ala Met Cys Gly Lys Arg Asp Cys Cys Val Pro Ala Asp Arg
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 Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile
 65 70 75 80

tca aca gta aca gca aca aca gca aca aca act ttg atg atg act act 288
 Ser Thr Val Thr Ala Thr Thr Ala Thr Thr Thr Leu Met Met Thr Thr
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Ala Ser Met Ser Ser Met Ala Pro Thr Arg Phe Ser His Trp Leu
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Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
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Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
 35 40 45

Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg
 50 55 60

Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile
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Ser Thr Val Thr Ala Thr Thr Ala Thr Thr Thr Leu Met Met Thr Thr
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